

SEQUENCE LISTING

<110> Ajinomoto Co., Inc.

<120> GENES INVOLVED IN POLYSACCHARIDE PRODUCTION AND
UTILIZATION THEREOF

<130> US-107

<150> JP 2003-32075

<151> 2003-02-10

<160> 13

<170> PatentIn Ver. 2.0

<210> 1

<211> 1404

<212> DNA

<213> *Methylophilus methylotrophus*

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<221> CDS

<222> (1).. (1404)

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ggg agt aat cca ctt tac atg ctt gag tct ctc gtt gag ccc ttg gtg 96
Gly Ser Asn Pro Leu Tyr Met Leu Glu Ser Leu Val Glu Pro Leu Val
           20           25           30
atg gtg ttt gtg ctg tgg ggg ttg ttt att tat acc gaa aac cgc att 144
Met Val Phe Val Leu Trp Gly Leu Phe Ile Tyr Thr Glu Asn Arg Ile
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ccg atg tcg att ttt att aca tcg ata gtg ctg ttt tcg att tct ttc 192

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Pro Ser Gly Ala Lys Ile Arg Lys Gly Phe Ala Lys Met Cys Arg Asp	
65 70 75 80	
gtg att ggt caa tgg ctg gtc att gcc acc ttt ttg ctg acc ttt gct	288
Val Ile Gly Gln Trp Leu Val Ile Ala Thr Phe Leu Leu Thr Phe Ala	
85 90 95	
tat atc act cgt tac atc acc tta tat agc gaa aaa tta att ctc gcc	336
Tyr Ile Thr Arg Tyr Ile Thr Leu Tyr Ser Glu Lys Leu Ile Leu Ala	
100 105 110	
tgg ttg att gtg acg cca gtt gcc cag att att gcg ttg cag tta cta	384
Trp Leu Ile Val Thr Pro Val Ala Gln Ile Ile Ala Leu Gln Leu Leu	
115 120 125	
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Lys Trp Ala Ser Pro Lys Leu Ile Glu Trp Gln Gly Pro Arg Gln Asn	
130 135 140	
acc ttg att atc ggc ttg aat gag caa ggt ctg ctt ttg gcg gat aat	480
Thr Leu Ile Ile Gly Leu Asn Glu Gln Gly Leu Leu Leu Ala Asp Asn	
145 150 155 160	
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Leu Lys Arg Asp Tyr Tyr Gln Arg Ile Asn Ile Leu Gly Phe Phe Glu	
165 170 175	
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Asp Arg Ala Pro Asn Arg Leu Pro His Ile Asp Ser Tyr Pro Val Leu	
180 185 190	
ggc agc ttg aat gaa ctg agt cat tac ctg aaa tca cac act gta cac	624
Gly Ser Leu Asn Glu Leu Ser His Tyr Leu Lys Ser His Thr Val His	
195 200 205	
aaa ctt tat atc gct tta ccg atg tcc agt cac cct cgt att ttg aaa	672
Lys Leu Tyr Ile Ala Leu Pro Met Ser Ser His Pro Arg Ile Leu Lys	
210 215 220	
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Leu Leu Asp Asp Leu Lys Asp Thr Thr Ala Ser Ile Tyr Phe Val Pro	
225 230 235 240	
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Asp Ile Phe Val Thr Asp Leu Ile Gln Gly Arg Val Ser Asp Val Asn	
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Gly Ile Pro Val Val Ser Val Cys Asp Thr Pro Phe Thr Gly Met Asp	
260 265 270	
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Gly Phe Ile Lys Arg Thr Ala Asp Ile Leu Phe Ser Leu Leu Val Leu	
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Ile Leu Ile Ser Pro Ile Leu Ile Gly Ile Ala Ile Ala Val Lys Leu	
290 295 300	
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Thr Ser Pro Gly Pro Val Ile Phe Lys Gln Arg Arg Tyr Gly Leu Asp	
305 310 315 320	
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Gly Gln Gln Ile Leu Val Tyr Lys Phe Arg Ser Met Thr Val Thr Glu	
325 330 335	
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340 345 350	
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Pro Leu Gly Ala Phe Leu Arg Lys Thr Ser Leu Asp Glu Leu Pro Gln	
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370 375 380	
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385 390 395 400	
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Met Val Arg His Lys Val Lys Pro Gly Ile Thr Gly Trp Ala Gln Val	
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aat ggc ttc cgc ggc gaa acg gac acg tta gaa aaa atg gag caa cgt	1296
Asn Gly Phe Arg Gly Glu Thr Asp Thr Leu Glu Lys Met Glu Gln Arg	
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Val His Tyr Asp Leu Glu Tyr Leu Arg Asn Trp Ser Pro Arg Leu Asp
435 440 445
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<213> Methylophilus methylotrophus

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Pro Met Ser Ile Phe Ile Thr Ser Ile Val Leu Phe Ser Ile Ser Phe
50 55 60
Pro Ser Gly Ala Lys Ile Arg Lys Gly Phe Ala Lys Met Cys Arg Asp
65 70 75 80
Val Ile Gly Gln Trp Leu Val Ile Ala Thr Phe Leu Leu Thr Phe Ala
85 90 95
Tyr Ile Thr Arg Tyr Ile Thr Leu Tyr Ser Glu Lys Leu Ile Leu Ala
100 105 110
Trp Leu Ile Val Thr Pro Val Ala Gln Ile Ile Ala Leu Gln Leu Leu
115 120 125
Lys Trp Ala Ser Pro Lys Leu Ile Glu Trp Gln Gly Pro Arg Gln Asn
130 135 140

Thr Leu Ile Ile Gly Leu Asn Glu Gln Gly Leu Leu Leu Ala Asp Asn
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Gly Ala Tyr
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<211> 1422

<212> DNA

<213> *Methylophilus methylotrophus*

<220>

<221> CDS

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Thr Arg Leu Trp Pro Leu Ser Arg Ala Val Leu Pro Lys Gln Leu Leu	
20 25 30	
cct ttg gtg acc gaa aat acg atg tta cag gag aca ttg atc cgg ctt	144
Pro Leu Val Thr Glu Asn Thr Met Leu Gln Glu Thr Leu Ile Arg Leu	
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Ser Ser Trp Ala Asp Val Gly His Pro Ile Val Val Cys Gly Asn Asp	
50 55 60	
cat cgc ttt ttg gtg gcg gag caa tta cgg caa gtg aat ttg aca cct	240
His Arg Phe Leu Val Ala Glu Gln Leu Arg Gln Val Asn Leu Thr Pro	
65 70 75 80	
gag gcg att gtg ctg gag ccg gtg gcg cga aat acg gca cct gcg att	288
Glu Ala Ile Val Leu Glu Pro Val Ala Arg Asn Thr Ala Pro Ala Ile	
85 90 95	
gct gct gcg gct gtg act tta aaa gac aaa gat gtc ttg atg ctg gtg	336
Ala Ala Ala Ala Val Thr Leu Lys Asp Lys Asp Val Leu Met Leu Val	

100	105	110	
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Leu Pro Ala Asp His Val Ile Thr Asp Val Thr Ala Phe Glu Ala Ala			
115	120	125	
gtg cgt cgt gcc tgc gtt gca gca gag cag ggg aaa ctg gtc aca ttt	432		
Val Arg Arg Ala Cys Val Ala Ala Glu Gln Gly Lys Leu Val Thr Phe			
130	135	140	
ggg ata gag cct aca cag cag gaa acc ggt tat ggt tat atc caa tca	480		
Gly Ile Glu Pro Thr Gln Pro Glu Thr Gly Tyr Gly Tyr Ile Gln Ser			
145	150	155	160
ggg gca gaa ttg gaa gca tgt gat ggt tgc ttt gaa gtg gca cgt ttt	528		
Gly Ala Glu Leu Glu Ala Cys Asp Gly Cys Phe Glu Val Ala Arg Phe			
165	170	175	
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Val Glu Lys Pro Asp Ala Ala Thr Ala Gln Gln Tyr Leu Asp Ala Gly			
180	185	190	
aac ttt tat tgg aac agc ggc atg ttt ttg ttt aaa ccg gct gtg ttc	624		
Asn Phe Tyr Trp Asn Ser Gly Met Phe Leu Phe Lys Pro Ala Val Phe			
195	200	205	
ctg gct gag ttg cag caa tac gcg cca gcc atg gtc agt gcg gta agc	672		
Leu Ala Glu Leu Gln Gln Tyr Ala Pro Ala Met Val Ser Ala Val Ser			
210	215	220	
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gag gcc tcg ttt gct gag tct cct tct gat tca att gac tat gcc gtc	768		
Glu Ala Ser Phe Ala Glu Ser Pro Ser Asp Ser Ile Asp Tyr Ala Val			
245	250	255	
atg gaa aaa acc aaa ctg gcg gcc gtg gta cct gcc agc atg ggg tgg	816		
Met Glu Lys Thr Lys Leu Ala Ala Val Val Pro Ala Ser Met Gly Trp			
260	265	270	
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290	295	300	
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Asn Thr Leu Val Arg Ala Glu Glu Arg Phe Val Ala Ala Val Gly Val			
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gag gat ttg ctg att gtt gaa acc agt gat gcg atc ctg gtt gcg cac	1008		
Glu Asp Leu Leu Ile Val Glu Thr Ser Asp Ala Ile Leu Val Ala His			
325	330	335	
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370	375	380	
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385	390	395	400
cgg gct gag cac tgg gtg gtt gtc agt ggg tct gcc atg atc act att	1248		
Arg Ala Glu His Trp Val Val Val Ser Gly Ser Ala Met Ile Thr Ile			
405	410	415	
gat gat gtc acc aag ctc tat act gaa aac gaa tct act tat ata ccg	1296		
Asp Asp Val Thr Lys Leu Tyr Thr Glu Asn Glu Ser Thr Tyr Ile Pro			
420	425	430	
att ggc tca acg cac cga cta gag aat cca ggt aaa ttg cct ttg cat	1344		
Ile Gly Ser Thr His Arg Leu Glu Asn Pro Gly Lys Leu Pro Leu His			
435	440	445	
tta atc gag gtg caa tcc ggt agt tat ctt gga gaa gat gac atc gtg	1392		
Leu Ile Glu Val Gln Ser Gly Ser Tyr Leu Gly Glu Asp Asp Ile Val			
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<212> PRT

<213> *Methylophilus methylotrophus*

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Pro	Leu	Val	Thr	Glu	Asn	Thr	Met	Leu	Gln	Glu	Thr	Leu	Ile	Arg	Leu
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Ser	Ser	Trp	Ala	Asp	Val	Gly	His	Pro	Ile	Val	Val	Cys	Gly	Asn	Asp
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His	Arg	Phe	Leu	Val	Ala	Glu	Gln	Leu	Arg	Gln	Val	Asn	Leu	Thr	Pro
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Glu	Ala	Ile	Val	Leu	Glu	Pro	Val	Ala	Arg	Asn	Thr	Ala	Pro	Ala	Ile
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Val	Arg	Arg	Ala	Cys	Val	Ala	Ala	Glu	Gln	Gly	Lys	Leu	Val	Thr	Phe
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Gly	Ile	Glu	Pro	Thr	Gln	Pro	Glu	Thr	Gly	Tyr	Gly	Tyr	Ile	Gln	Ser
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Gly	Ala	Glu	Leu	Glu	Ala	Cys	Asp	Gly	Cys	Phe	Glu	Val	Ala	Arg	Phe
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Val	Glu	Lys	Pro	Asp	Ala	Ala	Thr	Ala	Gln	Gln	Tyr	Leu	Asp	Ala	Gly
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Leu	Ala	Glu	Leu	Gln	Gln	Tyr	Ala	Pro	Ala	Met	Val	Ser	Ala	Val	Ser
				210				215				220			
Asn	Ala	Val	Ala	Gln	Ser	Tyr	Lys	Asp	Leu	Asp	Phe	Val	Arg	Leu	His
				225				230				235			240
Glu	Ala	Ser	Phe	Ala	Glu	Ser	Pro	Ser	Asp	Ser	Ile	Asp	Tyr	Ala	Val

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Met	Glu	Lys	Thr	Lys	Leu
				Ala	Ala
			Val	Val	Pro
				Ala	Ser
				Met	Gly
				Trp	
	260		265		270
Asn	Asp	Val	Gly	Ser	Trp
				Thr	Ala
				Leu	Lys
				Glu	Val
				Gln	Pro
				Asn	Asp
	275		280		285
Ala	Asp	Gly	Asn	Ala	Thr
				Arg	Gly
				Asp	Val
				Phe	Leu
				Lys	Asn
				Val	Lys
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Asn	Thr	Leu	Val	Arg	Ala
				Glu	Glu
				Arg	Phe
				Val	Ala
				Ala	Val
				Gly	Val
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					320
Glu	Asp	Leu	Leu	Ile	Val
				Glu	Thr
				Ser	Asp
				Ala	Ile
				Leu	Val
				Ala	His
	325		330		335
Arg	Asp	Cys	Ala	Gln	Asp
				Val	Lys
				Asn	Ile
				Val	Asp
				His	Leu
				Lys	Ala
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Ser	Gly	Arg	Ser	Glu	His
				Lys	Met
				His	Pro
				Arg	Val
				Tyr	Arg
				Pro	Trp
	355		360		365
Gly	Trp	Tyr	Glu	Gly	Ile
				Asp	Ile
				Gly	Glu
				Arg	Phe
				Gln	Val
				Lys	Arg
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Ile	Met	Val	Lys	Pro	Gly
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				Leu	Ser
				Leu	Gln
				Met	His
				His	His
	385		390		395
					400
Arg	Ala	Glu	His	Trp	Val
				Val	Val
				Ser	Gly
				Ser	Ala
				Met	Ile
				Thr	Ile
	405		410		415
Asp	Asp	Val	Thr	Lys	Leu
				Tyr	Thr
				Glu	Asn
				Glu	Ser
				Thr	Tyr
				Ile	Pro
	420		425		430
Ile	Gly	Ser	Thr	His	Arg
				Leu	Glu
				Asn	Pro
				Gly	Lys
				Leu	Pro
				Leu	His
	435		440		445
Leu	Ile	Glu	Val	Gln	Ser
				Gly	Ser
				Tyr	Leu
				Gly	Glu
				Asp	Asp
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Arg	Phe	Glu	Asp	Thr	Tyr
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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer MgtfA-F1

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<213> Artificial Sequence

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<212> DNA

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<223> Description of Artificial Sequence: primer Km4-R2

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<210> 9

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer Km4-R1

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer mManC-F1

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<210> 11

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<210> 12

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<212> DNA

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<223> Description of Artificial Sequence: primer mManC-F2

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer mManC-R2

<400> 13

tcgtgacata gcgttgacaca tagccotcat a

31